Reynolds Lab Notebook Policy

Your lab notebook is a legal document, and provides a clear record of your research in the lab. It must be sufficient to enable anyone else in the lab to repeat your experimental results. We keep our lab notebooks electronically using Benchling:
https://benchling.com/organizations/reynoldslab/projects

Ultimately the best lab notebook organization is one that you can follow, regularly update, and that is understandable by your labmates and Kim. Individual lab notebook styles may vary, but here are a few important organizational rules to keep in mind.

- Within the Reynolds Lab group on Benchling, please organize your work by project. A project should represent a roughly publication-sized unit of work, the expectation is that graduate students might have 2-3 projects during their time in the lab.

- You should also create and maintain a benchling project for any computational-only work. This is NOT the place to put code, but rather to document your process – things you tried, what worked, what didn't and screen shots of key plots demonstrating results or things you are troubleshooting. This might include steps you followed to set up a particular compute environment, parameter combinations you tried in a particular modeling or fitting strategy, or your strategy for configuring a particular program. Having a record of your computational processes can be just as important as for your experiments.

- Projects should be named according to the following convention. We have four benchling project types:

  Rotation

  Rotation: YY FirstLast ProjectTitle

  The year (YY) should indicate initial creation. This will let us sort things (approximately) chronologically within each project type.

  Outside lab collaboration

  Collab: YY LabName ProjectTitle

  Specific Project

  Proj: YY FirstLast ProjTitle

  For the project title – be specific. Avoid jargon (like specific plasmid names, Kim won't know what these are years later). Projects (and project titles) should be centered around particular scientific problems/questions (e.g a unit of publication), not a technique (e.g. "Developing Genomic DHFR Complementation Assay", not "ORBIT")

  Once a project has been completed (say we publish a paper, or decide that a particular approach isn't working and we want to shelve it), the project name will be updated to have a "X" put in front of it (XProj: YY FirstlLast ProjTitle). This way, completed or shelved projects will sort to the bottom of the list in their own section.

Lab member specific protocols/vector maps/ materials

GenMat: YY FirstLast

The idea is to consolidate into a single project any data/methods/etc related to “general lab stuff” on a per-user basis. Possible subfolders for this kind of project might include lab member specific directories like: archive, protocols, plasmid maps, rotation projects/misc

- Within your project, include a base-level entry that is roughly equivalent to a README. This entry should have a 1-2 paragraphs describing the general goals of the project, and a table of contents referring to any subfolders. When the project transitions to “XProj” (closed) there should be an additional sentence or short paragraph summarizing outcome. (“This project was published as blah-blah” Or “While we successfully constructed a series of light inducible plasmids, we found that none had sufficient dynamic range of induction to reliably control sgRNA expression”)
- Remaining entries within a project should be organized into subfolders. You may wish to have subfolders that correspond to particular techniques (“NMR of DHFR/LOV2 DL121 fusion”, “Enzyme kinetics for DHFR”), or subproject (“cloning of DHFR thermal stability variants”)
- Keep in mind that access/sharing is at the project level. If you and a lab mate are working together on something, it may make sense to create a new project for this collaboration.
- Include all the data!!! Don’t leave out negative results, mistakes, or errors, just note them clearly. Did you mis-pour a sleeve of plates? Write it down. Did you protein prep crash? ABSOLUTELY write it down. Did you set up a PCR and then had no bands? ABSOLUTELY write it down. Failed experiments are invaluable in figuring out what works.
- Often lab members make paper/pencil notes while doing an experiment. Checklists on paper towels, handwritten protocol modifications, sticky notes, crystallography screening notes, etc should all be scanned/photographed and included. Please do not forget to capture relevant information about how your experiment was done.
- Time is an important and often overlooked aspect of experiments: particularly when making fitness measurements. Make sure to note when you put in overnights, when you started an adaptation step, etc.
- Record lot numbers for enzymes (including polymerase)
- Photographs/gel images should be labeled to indicate bands and relevant molecular weights.
- Much of the data collected in our lab requires additional computational analysis for interpretation. It is not necessary to include ALL of your data analysis in Benchling. However it is expected that you will include any graphs/tables or processed data that are necessary to interpret if your experiment worked. For example, Michaelis Menten progress curves and steady state parameter fits should be included. For a MiSeq experiment, you should include cluster density, fraction of reads passing filter, and a bargraph showing how reads are distributed amongst any multiplexed samples.

- We also maintain a set of lab standard protocols under the shared project “Reynolds Lab Shared Materials” . Lab standard protocols are flagged (in the title) by the prefix ‘KRlab_’. Lab standard protocols should be created for methods or reagent prep in the lab that extends to more than two people. Any proposed revisions should be reviewed by at least one other lab member prior to implementation.

- The Benchling notebooks are exported and archived quarterly on the BioHPC. Archived copies will be kept for at least five years, the cloud version will persist indefinitely